REMARKS

The above amendments have been made in compliance with the sequence listing requirements. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached pages are captioned "**Version With Markings To Show Changes Made**."

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION

The paragraph beginning at page 2, line 18:

Fig 1: Multiple alignment of superantigen protein sequences (SEQ ID NOS:9, 2, 8, 10, 4 and 6, respectively, in order of appearance).

The paragraph beginning at page 5, line 11:

Figure 1 (SEQ ID NOS:9, 2, 8, 10, 4 and 6, respectively, in order of appearance) shows the amino acid sequences of the above four superantigens together with those of previously identified superantigens SMEZ, SPE-C and SEA.

The paragraph beginning at page 5, line 26:

The most significant difference between SMEZ and SMEZ-2 is an exchanged pentapeptide sequence at position 96-100, where the EEPMS (SEQ ID NO:9) sequence of SMEZ is converted to KTSIL (SEQ ID NO:2) in SMEZ-2 (Fig. 1). A second difference is at position 111-112, where an RR dipeptide is exchanged for GK in SMEZ-2. The remaining 10 different residues are spread over almost the entire primary sequence.

The following paragraph beginning at page 5, line 31:

Figure 2 (SEQ ID NOS:1-2) shows the nucleotide sequence encoding mature SMEZ-2 and the deduced amino acid sequence.

The paragraph beginning at page 6, line 1:

Likewise, Figures 3 to 5 (SEQ ID NOS:3-8) show the nucleotide sequence encoding mature SPE-G, SPE-H and SPE-J superantigens, respectively, together with their respective deduced amino acid sequences.

The paragraph beginning at page 6, line 6:

The invention is of course not restricted to superantigens/polynucleotides having the specific sequences of Figures 1 to 5 (SEQ ID NOS:1-11). Instead, functionally equivalent variants are contemplated.

The paragraphs beginning at page 15, line 5:

Fifty nanograms of *S.pyogenes* M1 (ATCC 700294) or *S.pyogenes* 2035 genomic DNA was used as a template to amplify the smez DNA fragment and the smez-2 DNA fragment, respectively, by PCR using the primers

smez-forward (TGGGATCCTTAGAAGTAGATAATA) (SEQ ID NO:12) and

smez-reverse (AAGAATTCTTAGGAGTCAATTTC) (SEQ ID NO:13) and Taq Polymerase (Promega). The primers contain a terminal tag with the restriction enzyme recognition sequences BamHI and EcoRI, respectively. The amplified DNA fragment, encoding the mature protein without the leader sequence

(Kamezawa et al, 1997 Infect. Immun. 65 no.9:38281-33) was cloned into a T-tailed pBlueScript SKII vector (Stratagene).

Spe-g and spe-h were cloned in similar approach, using the primers spe-g-fw

(CTGGATCCGATGAAAATTTAAAAGATTTAA) (SEQ ID NO:14) and spe-g-rev (AAGAATTCGGGGGGAGAATAG), (SEQ ID NO:15) and primers spe-h-fw (TTGGATCCAATTCTTATAATACAACC) (SEQ ID NO:16) and spe-h-rev (AAAAGCTTTTAGCTGATTGACAC), (SEQ ID NO:17) respectively.

The paragraph beginning at page 19, line 27:

The most significant difference between SMEZ and SMEZ-2 is an exchanged pentapeptide sequence at position 96-100, where the EEPMS (SEQ ID NO:9) sequence of SMEZ is converted to KTSIL (SEQ ID NO:2) in SMEZ-2 (Fig. 1). A second cluster is at position 111-112, where an RR dipeptide is exchanged for GK in SMEZ-2. The remaining 10 different residues are spread over almost the entire primary sequence.

The paragraph beginning at page 20, line 15:

Multiple alignment of SAg protein sequences (Fig. 1) (SEQ ID NOS:9, 2, 8, 10, 4 and 6, respectively, in order of appearance) shows that similarities are clustered within structure determining regions, represented by α4, α5, β4 and β5

regions. This applies to all toxins of the superantigen family (data not shown) and explains why superantigens like SPE-C and SEA have very similar overall structures despite their rather low sequence identity of 24.4%.

The paragraph beginning at page 29, line 34:

Purified genomic DNA from all *Str. Pyogenes* isolates was used for PCR with specific primers for the smez, spe-g and spe-h genes as described above and by Proft (1999). In addition, a primer pair specific to a DNA region encoding the 23S, rRNA, oligo 23rRNA forward (SEQ ID NO:18) (GCTATTTCGGAGAGAACCAG) and oligo 23rRNA reverse (SEQ ID NO:19) (CTGAAACATCTAAGTAGCTG) was designed and used for PCR as a positive control.